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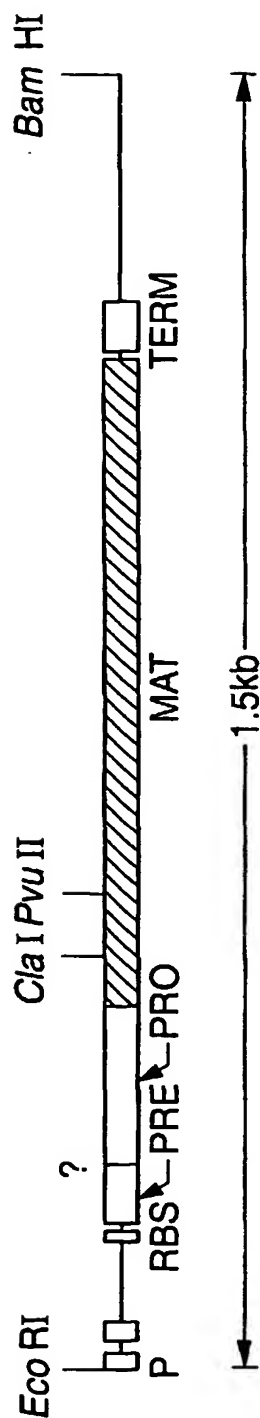


FIG. 1A

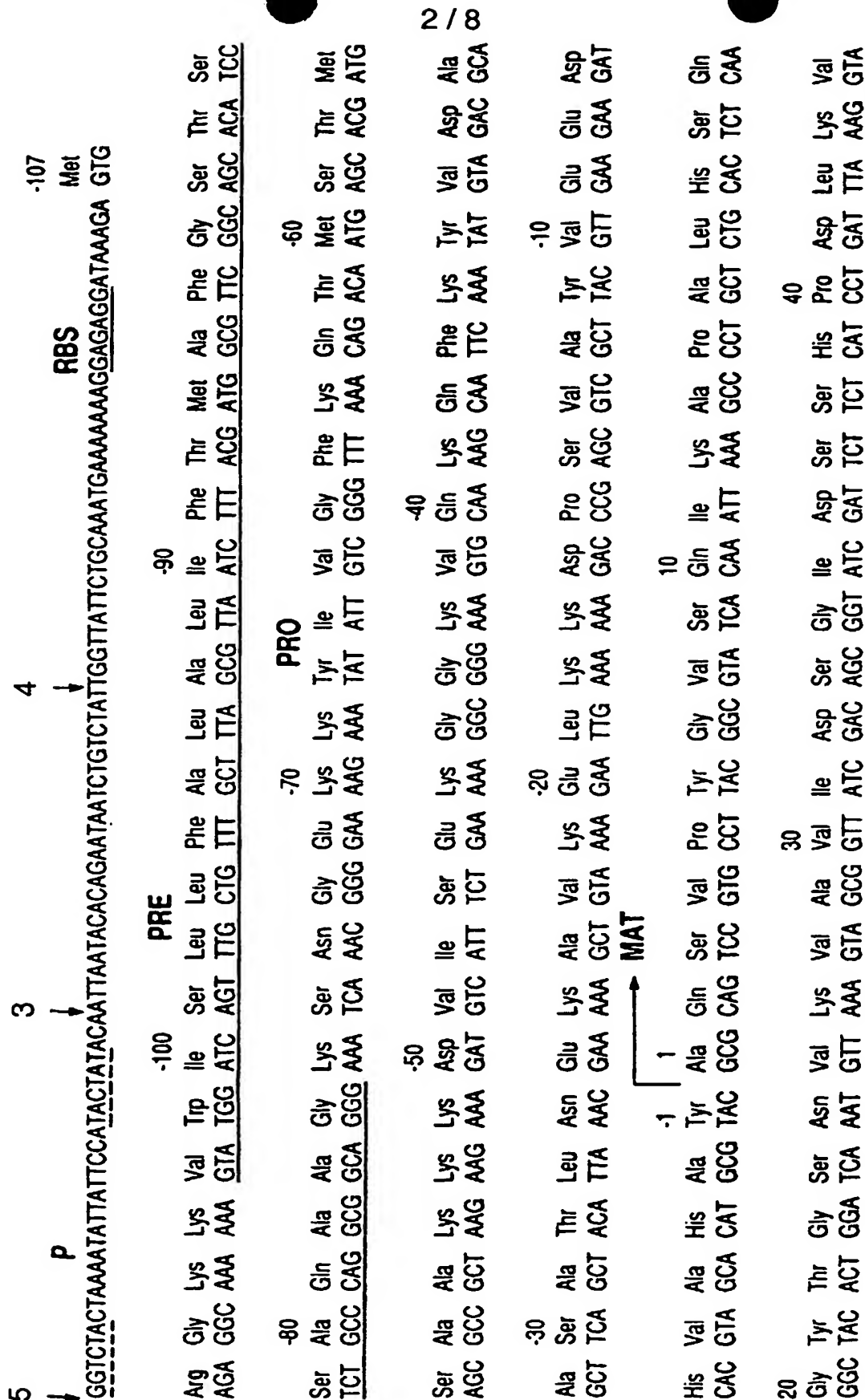


FIG. 1B - 1

	Ala	Gly	Gly	Ala	Ser	Met	Val	Pro	Ser	Glu	Thr	Asn	Pro	Phe	Gln	Asp	Asn	Asp	Ser	His	Gly	Thr	His	Val	Ala	
549	GCA	GGC	GGA	GCC	AGC	ATG	GTT	CCT	TCT	TCT	GAA	ACA	AAT	CCT	TTC	CAA	GAC	AAC	AAC	TCT	CAC	GGA	ACT	CAC	GTT	GCC

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Conserved Residues in Subtilisins from
Bacillus Amyloliquefaciens

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1           10           20
A Q S V P . G . . . . A P A . H . . G

21           30           40
. T G S . V K V A V . D . G . . . . H P

41           50           60
D L . . . G G A S . V P . . . . . Q D

61           70           80
. N . H G T H V A G T . A A L N N S I G

81           90           100
V L G V A P S A . L Y A V K V L G A . G

101          110          120
S G . . S . L . . G . E W A . N . . . .

121          130          140
V . N . S L G . P S . S . . . . . A . .

141          150          160
. . . . . G V . V V A A . G N . G . . .

161          170          180
. . . . . Y P . . Y . . . . A V G A .

181          190          200
D . . N . . A S F S . . G . . L D . . A

201          210          220
P G V . . Q S T . P G . . Y . . . . N G T

221          230          240
S M A . P H V A G A A A L . . . K . . .

241          250          260
W . . . Q . R . . L . N T . . . L G . .

261          270
. . Y G . G L . N . . A A . .

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FIG._2

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COMPARISON OF SUBTILISIN SEQUENCES FROM:

*B.amyloliquefaciens**B.subtilis**B.licheniformis**B.lentus***FIG._3A**

01	10	20	30	
A Q S V P Y G V S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P				
A Q S V P Y G I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P				
A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P				
A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T * H P				
41	50	60	70	
D L K V A G G A S M V P S E T N P P Q D N N S H G T H V A G T V A A L N N S I G				
D L N V R G G A S P V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I G				
D L N V V G G A S P V A G E A Y N * T D G N G H G T H V A G T V A A L D N T T G				
D L N I R G G A S P V P G E E * P S T Q D G N G H G T H V A G T I A A L N N S I G				
81	90	100	110	
V L G V A P S A S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D				
V L G V S P S A S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D				
V L G V A P S V S L Y A V K V L N S S G S G S Y S G I V S G I E W A T N G M D				
V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N N G M H				
121	130	140	150	
V I N M S L G G P S G S A A L K A A V D K A V A S G V V V A A A A G N E G T S G				
V I N M S L G G P T G S T A L K K T V V D K A V S S G I V V A A A A G N E G S S G				
V I N M S L G G A S G S T A M K Q A V D N A Y A R G V V V A A A A G N S G N S G				
V A N L S L G S P S A T L E Q A V N S A T S R G V L V A A S G N S G A G S				

161
 S S S T V G Y P G K Y P S V I A V G A V D S S N Q R A S F S S V G P E L D V M A
 S S S T V G Y P A K Y P S T I A V G A V N S S N Q R A S F S S V G S E L D V M A
 S S T N T I G Y P A K Y P S V I A V G A V D S S N S N R A S F S S V G A E L E V M A
 * * * I S Y P A R Y A N A M A V G A T D Q N N R A S F S S Q Y G A G L D I V A

201
 P G V S I Q S T L P G N K Y G A Y N G T S M A S P H V A G A A A L I L S K H P N
 P G V S I Q S T L P G G T Y G A Y N G T S M A T P H V A G A A A L I L S K H P T
 P G A G V Y S T Y P T N T Y A T L N G T S M A S P H V A G A A A L I L S K H P N
 P G V N V Q S T Y P G S T Y A S L N G T S M A T P H V A G A A A L V K K N P S

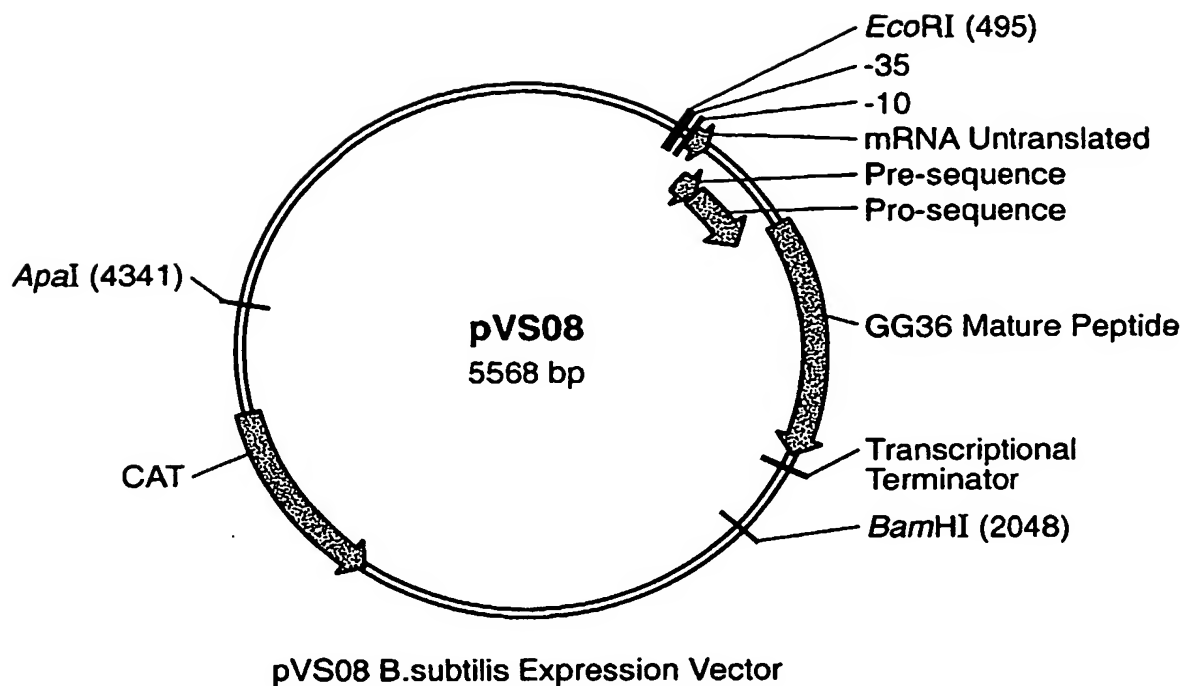
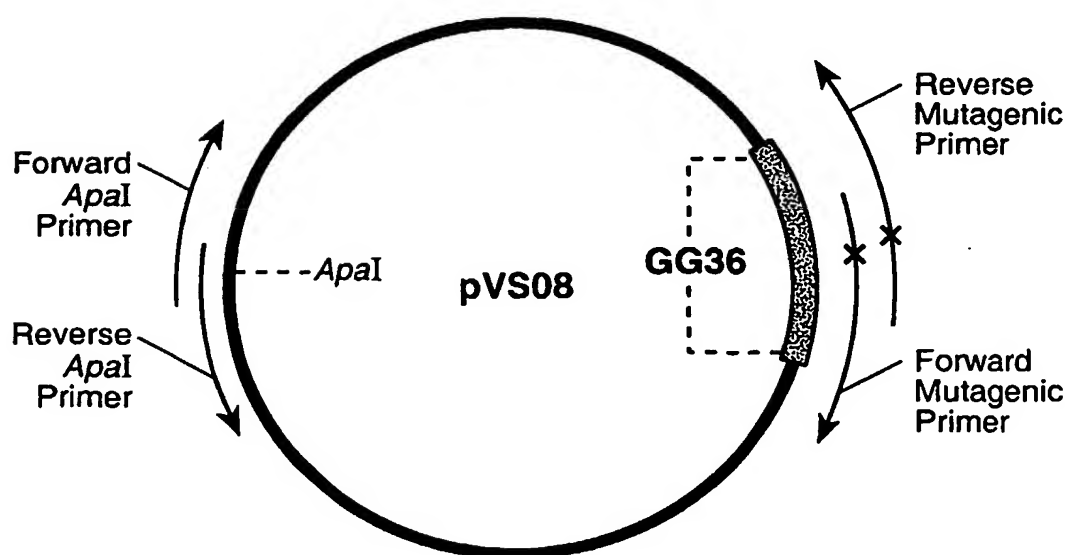
241
 W T N T Q V R S S L E N T T K L G D S F Y Y G K G L I N V Q A A A Q
 W T N A Q V R D R R L E S T A T Y L G N S F Y Y G K G L I N V Q A A A Q
 L S A S Q V R R N R L S S T A T Y L G S S F Y Y G K G L I N V E A A A Q
 W S N V Q I R N H L K N T A T S L G S T N L Y G S G L V N A E A A T R

FIG.-3B

FIG.-3A

FIG.-3B

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**FIG._4****FIG._5**